

1  
SEQUENCE LISTING

<110> SmithKline Beecham Corporation  
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Wisely, Bruce  
Collins, Jon

<120> CAR LIGAND-BINDING DOMAIN POLYPEPTIDE CO-CRYSTALLIZED WITH A  
LIGAND, AND METHODS OF DESIGNING LIGANDS THAT MODULATE CAR  
ACTIVITY

<130> PR60235

<150> 60/488,415  
<151> 2003-07-18

<160> 7

<170> PatentIn version 3.2

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tccaatcact ggcaactcct gagatcagag gaaaaccagc aacagcgtgg gagtttgggg 180  
agaggcattc cataccagat tctgtggcct gcagggtgaca tgctgcctaa gagaagcagg 240  
agtctgtgac agccacccca acacgtgacg tc atg gcc agt agg gaa gat gag 293  
Met Ala Ser Arg Glu Asp Glu  
1 5  
ctg agg aac tgt gtg gta tgt ggg gac caa gcc aca ggc tac cac ttt 341  
Leu Arg Asn Cys Val Val Cys Gly Asp Gln Ala Thr Gly Tyr His Phe  
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aat gcg ctg act tgt gag ggc tgc aag ggt ttc ttc agg aga aca gtc 389  
Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Val  
25 30 35  
agc aaa agc att ggt ccc acc tgc ccc ttt gct gga agc tgt gaa gtc 437  
Ser Lys Ser Ile Gly Pro Thr Cys Pro Phe Ala Gly Ser Cys Glu Val  
40 45 50 55  
agc aag act cag agg cgc cac tgc cca gcc tgc agg ttg cag aag tgc 485  
Ser Lys Thr Gln Arg Arg His Cys Pro Ala Cys Arg Leu Gln Lys Cys  
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tta gat gct ggc atg agg aaa gac atg ata ctg tcg gca gaa gcc ctg 533  
Leu Asp Ala Gly Met Arg Lys Asp Met Ile Leu Ser Ala Glu Ala Leu

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Ala	Leu	Arg	Arg	Ala	Lys	Gln	Ala	Gln	Arg	Arg	Ala	Gln	Gln	Thr	Pro	
		90					95					100				
gtg	caa	ctg	agt	aag	gag	caa	gaa	gag	ctg	atc	cgg	aca	ctc	ctg	ggg	629
Val	Gln	Leu	Ser	Lys	Glu	Gln	Glu	Glu	Leu	Ile	Arg	Thr	Leu	Leu	Gly	
	105					110					115					
gcc	cac	acc	cgc	cac	atg	ggc	acc	atg	ttt	gaa	cag	ttt	gtg	cag	ttt	677
Ala	His	Thr	Arg	His	Met	Gly	Thr	Met	Phe	Glu	Gln	Phe	Val	Gln	Phe	
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agg	cct	cca	gct	cat	ctg	ttc	atc	cat	cac	cag	ccc	ttg	ccc	acc	ctg	725
Arg	Pro	Pro	Ala	His	Leu	Phe	Ile	His	His	Gln	Pro	Leu	Pro	Thr	Leu	
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gcc	cct	gtg	ctg	cct	ctg	gtc	aca	cac	ttc	gca	gac	atc	aac	act	ttc	773
Ala	Pro	Val	Leu	Pro	Leu	Val	Thr	His	Phe	Ala	Asp	Ile	Asn	Thr	Phe	
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atg	gta	ctg	caa	gtc	atc	aag	ttt	act	aag	gac	ctg	ccc	gtc	ttc	cgt	821
Met	Val	Leu	Gln	Val	Ile	Lys	Phe	Thr	Lys	Asp	Leu	Pro	Val	Phe	Arg	
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tcc	ctg	ccc	att	gaa	gac	cag	atc	tcc	ctt	ctc	aag	gga	gca	gct	gtg	869
Ser	Leu	Pro	Ile	Glu	Asp	Gln	Ile	Ser	Leu	Leu	Lys	Gly	Ala	Ala	Val	
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gaa	atc	tgt	cac	atc	gta	ctc	aat	acc	act	ttc	tgt	ctc	caa	aca	caa	917
Glu	Ile	Cys	His	Ile	Val	Leu	Asn	Thr	Thr	Phe	Cys	Leu	Gln	Thr	Gln	
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Asn	Phe	Leu	Cys	Gly	Pro	Leu	Arg	Tyr	Thr	Ile	Glu	Asp	Gly	Ala	Arg	
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Val	Gly	Phe	Gln	Val	Glu	Phe	Leu	Glu	Leu	Leu	Phe	His	Phe	His	Gly	
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Thr	Leu	Arg	Lys	Leu	Gln	Leu	Gln	Glu	Pro	Glu	Tyr	Val	Leu	Leu	Ala	
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gcc	atg	gcc	ctc	ttc	tct	cct	gac	cga	cct	gga	gtt	acc	cag	aga	gat	1109
Ala	Met	Ala	Leu	Phe	Ser	Pro	Asp	Arg	Pro	Gly	Val	Thr	Gln	Arg	Asp	
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Glu	Ile	Asp	Gln	Leu	Gln	Glu	Glu	Met	Ala	Leu	Thr	Leu	Gln	Ser	Tyr	
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Ile	Lys	Gly	Gln	Gln	Arg	Arg	Pro	Arg	Asp	Arg	Phe	Leu	Tyr	Ala	Lys	
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ttg	cta	ggc	ctg	ctg	gct	gag	ctc	cgg	agc	att	aat	gag	gcc	tac	ggg	1253
Leu	Leu	Gly	Leu	Leu	Ala	Glu	Leu	Arg	Ser	Ile	Asn	Glu	Ala	Tyr	Gly	
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tac caa atc cag cac atc cag ggc ctg tct gcc atg atg ccg ctg ctc 1301  
 Tyr Gln Ile Gln His Ile Gln Gly Leu Ser Ala Met Met Pro Leu Leu  
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cag gag atc tgc agc tgaggccatg ctccacttcct tccccagctc acctggaaca 1356  
 Gln Glu Ile Cys Ser  
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Gly Phe Phe Arg Arg Thr Val Ser Lys Ser Ile Gly Pro Thr Cys Pro  
 35 40 45

Phe Ala Gly Ser Cys Glu Val Ser Lys Thr Gln Arg Arg His Cys Pro  
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Ala Cys Arg Leu Gln Lys Cys Leu Asp Ala Gly Met Arg Lys Asp Met  
 65 70 75 80

Ile Leu Ser Ala Glu Ala Leu Ala Leu Arg Arg Ala Lys Gln Ala Gln  
 85 90 95

Arg Arg Ala Gln Gln Thr Pro Val Gln Leu Ser Lys Glu Gln Glu Glu  
 100 105 110

Leu Ile Arg Thr Leu Leu Gly Ala His Thr Arg His Met Gly Thr Met  
 115 120 125

Phe Glu Gln Phe Val Gln Phe Arg Pro Pro Ala His Leu Phe Ile His  
 130 135 140

His Gln Pro Leu Pro Thr Leu Ala Pro Val Leu Pro Leu Val Thr His  
 145 150 155 160

Phe Ala Asp Ile Asn Thr Phe Met Val Leu Gln Val Ile Lys Phe Thr  
 165 170 175

4

Lys Asp Leu Pro Val Phe Arg Ser Leu Pro Ile Glu Asp Gln Ile Ser  
 180 185 190

Leu Leu Lys Gly Ala Ala Val Glu Ile Cys His Ile Val Leu Asn Thr  
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Thr Phe Cys Leu Gln Thr Gln Asn Phe Leu Cys Gly Pro Leu Arg Tyr  
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Thr Ile Glu Asp Gly Ala Arg Val Gly Phe Gln Val Glu Phe Leu Glu  
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Leu Leu Phe His Phe His Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu  
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Pro Glu Tyr Val Leu Leu Ala Ala Met Ala Leu Phe Ser Pro Asp Arg  
 260 265 270

Pro Gly Val Thr Gln Arg Asp Glu Ile Asp Gln Leu Gln Glu Glu Met  
 275 280 285

Ala Leu Thr Leu Gln Ser Tyr Ile Lys Gly Gln Gln Arg Arg Pro Arg  
 290 295 300

Asp Arg Phe Leu Tyr Ala Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg  
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Ser Ile Asn Glu Ala Tyr Gly Tyr Gln Ile Gln His Ile Gln Gly Leu  
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96

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Gly Ala His Thr Arg His Met Gly Thr Met Phe Glu Gln Phe Val Gln  
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ttt agg cct cca gct cat ctg ttc atc cat cac cag ccc ttg ccc acc 144  
 Phe Arg Pro Pro Ala His Leu Phe Ile His His Gln Pro Leu Pro Thr  
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ctg gcc cct gtg ctg cct ctg gtc aca cac ttc gca gac atc aac act 192  
 Leu Ala Pro Val Leu Pro Leu Val Thr His Phe Ala Asp Ile Asn Thr  
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ttc atg gta ctg caa gtc atc aag ttt act aag gac ctg ccc gtc ttc 240  
 Phe Met Val Leu Gln Val Ile Lys Phe Thr Lys Asp Leu Pro Val Phe  
                   65                  70                  75                  80

cgt tcc ctg ccc att gaa gac cag atc tcc ctt ctc aag gga gca gct 288  
 Arg Ser Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly Ala Ala  
                   85                  90

gtg gaa atc tgt cac atc gta ctc aat acc act ttc tgt ctc caa aca 336  
 Val Glu Ile Cys His Ile Val Leu Asn Thr Thr Phe Cys Leu Gln Thr  
                   100                  105

caa aac ttc ctc tgc ggg cct ctt cgc tac aca att gaa gat gga gcc 384  
 Gln Asn Phe Leu Cys Gly Pro Leu Arg Tyr Thr Ile Glu Asp Gly Ala  
                   115                  120                  125

cgt gtg ggg ttc cag gta gag ttt ttg gag ttg ctc ttt cac ttc cat 432  
 Arg Val Gly Phe Gln Val Glu Phe Leu Glu Leu Leu Phe His Phe His  
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gga aca cta cga aaa ctg cag ctc caa gag cct gag tat gtg ctc ttg 480  
 Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu Pro Glu Tyr Val Leu Leu  
                   145                  150                  155                  160

gct gcc atg gcc ctc ttc tct cct gac cga cct gga gtt acc cag aga 528  
 Ala Ala Met Ala Leu Phe Ser Pro Asp Arg Pro Gly Val Thr Gln Arg  
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gat gag att gat cag ctg caa gag gag atg gca ctg act ctg caa agc 576  
 Asp Glu Ile Asp Gln Leu Gln Glu Glu Met Ala Leu Thr Leu Gln Ser  
                   180                  185                  190

tac atc aag ggc cag cag cga agg ccc cgg gat cgg ttt ctg tat gcg 624  
 Tyr Ile Lys Gly Gln Gln Arg Arg Pro Arg Asp Arg Phe Leu Tyr Ala  
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 Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg Ser Ile Asn Glu Ala Tyr  
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ggg tac caa atc cag cac atc cag ggc ctg tct gcc atg atg 714  
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Phe Arg Pro Pro Ala His Leu Phe Ile His His Gln Pro Leu Pro Thr  
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Leu Ala Pro Val Leu Pro Leu Val Thr His Phe Ala Asp Ile Asn Thr  
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Phe Met Val Leu Gln Val Ile Lys Phe Thr Lys Asp Leu Pro Val Phe  
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Arg Ser Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly Ala Ala  
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Val Glu Ile Cys His Ile Val Leu Asn Thr Thr Phe Cys Leu Gln Thr  
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Gln Asn Phe Leu Cys Gly Pro Leu Arg Tyr Thr Ile Glu Asp Gly Ala  
 115 120 125

Arg Val Gly Phe Gln Val Glu Phe Leu Glu Leu Leu Phe His Phe His  
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Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu Pro Glu Tyr Val Leu Leu  
 145 150 155 160

Ala Ala Met Ala Leu Phe Ser Pro Asp Arg Pro Gly Val Thr Gln Arg  
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Asp Glu Ile Asp Gln Leu Gln Glu Glu Met Ala Leu Thr Leu Gln Ser  
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Tyr Ile Lys Gly Gln Gln Arg Arg Pro Arg Asp Arg Phe Leu Tyr Ala  
 195 200 205

Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg Ser Ile Asn Glu Ala Tyr  
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site

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